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Genetic analysis for estimates components of genetic variance in Indian mustard (*Brassica juncea* (L.) Czern & Coss)

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Abstract
Highly significant differences were recorded among the treatments for all the characters. Analysis of variance further indicated highly significant differences among the parents, F_{1s} and parent vs F_{1s} for all the characters. The estimates of all genetic components were found highly significant for Days to flowering, Days to maturity, plant height, length of main raceme, number of siliquae per plant, number of secondary branches per plant, oil content, test weight and seed yield per plant. The estimates of mean degree of dominance were more than unity for length of main raceme, number of secondary branches per plant oil content, test weight and seed yield per. The proportion of genes with positive and negative effects were near or equal to theoretical value for all the nine characters.

Keywords: Brassica, genetic components and gene action.

1. Introduction
Indian mustard [*Brassica juncea* (L.) Czern & Coss] is the dominant species covering around 85 per cent of area under rapeseed mustard in India. The rest of the area is covered by three ecotypes of *Brassica rapa* variety brown sarson, yellow sarson and toria. Among the toria [*Brassica rapa* (L.) spp. Toria] nearly 1.4% area. *Eruca sativa*. *Brassica rapa* L. spp. brown sarson and other occupy nearly 6 percent of the total area. Regarding the origin of Indian mustard [*Brassica juncea*] there are two opinions put forwarded for its origin. According to the species has originated in middle east where the putative parental species *Brassica campestris* and *Brassica nigra* might have first came into contact argued that *Brassica juncea* has probably arisen by hybridization between different *Bassica campestris* and *Brassica nigra* genotypes at different times and localities resulting in secondary centres of origin in China, North- Western India and the Caucasus. Rapeseed mustard oil is used primarily for edible purposes and is the principal cooking oil in the mustard growing areas of the country. Besides, seeds are used as condiments and in preparations of salad, juices, curries and pickles. The meal cake left after oil extracting forms on important cattle feed and may also be used as organic manure.

2. Materials & Methods
The material for the present investigation consisted seven varieties/ genotypes of Indian mustard, [*Brassica juncea* (L.) Czern & Coss] which were selected on the basis of variation for various characters from available genetic material. Using seven diverse genotypes, a diallel set (excluding reciprocals) was made to obtain 21 crosses during *Rabi*, 2009-2010. Plan of layout- All the 28 treatments, (7 parents and 21 F_1s) were grown in randomized complete block design with three replications at Oilseed Research Farm, Kalyanpur, C.S. Azad University of Agriculture and Technology, Kanpur during Rabi 2010-2011. The parents and F_1s were grown in single row of five meter length spaced 45 cm apart. The distance of 20 cm between the plants in a row was maintained by thinning. All the recommended agronomic practices were followed for raising the good crop. The following observations were recorded on 5 randomly taken plants in parents and F_1s in each replication namely, days to 50% flowering, days to maturity, plant height (cm), length of main raceme (cm), number of siliquae per plant, number of secondary branches per plant, oil content (%), test weight (g) and seed yield per plant (g). Diallele neumerical approach was suggested by Griffings in 1956. Oil content is estimated by using NMR Spectro 4000**.**

3. Results & Discussion
The analysis of variance was carried out for nine characters for testing the significance of

Differences amongst the genotypes are presented in table-1. Highly significant differences were recorded among the treatments for all the characters namely, days to flowering, Days to maturity, plant height, length of main raceme, number of siliquae per plant, number of secondary branches per plant, oil content, test weight and seed yield per plant. Analysis of variance further indicated highly significant differences among the parents. Highly significant differences were also found among F_1s for all the nine characters, parent vs. F_1s revealed highly significant differences for the characters, plant height, length of main raceme per plant, number of siliquae per plant. These findings were also similar as Aruna chalam (1976) [1] and Yadav *et al*. (1993) [10].

Analysis of components was carried out for all the nine characters in F_1 generations are presented in table-2. Regression coefficient 'b_1' deviated from unity for length of main raceme, Number of secondary branches per plant, test weight, oil content, Number of siliquae per plant, seed yield per plant. Such significant deviation of regression coefficient from unity indicates non-allelic gene interaction (epistasis), while the regression coefficient did not deviate significantly from unity for Plant height, Days to flowering, days to maturity, indicating the involvement of additive gene action. The finding were also suggested by Kumar and Srivastava (2000), Ghosh and Gulati (2001), Ghosh *et al*. (2002) [4], Singh and Sachan (2003), Sheikh and Singh (2004) [9], Goswami and Behl (2005) [5], Singh *et al*. (2007) [15].

The estimates of all genetic components viz., $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{F}$, $\hat{h}^2$ and $\hat{E}$ along with their standard errors were calculated. These estimates are presented in table-3. The estimates of additive components were highly significant for Days to flowering, Days to maturity, plant height, length of main raceme, number of siliquae per plant, number of secondary branches per plant, oil content, test weight and seed yield per plant. The estimated dominance components ($\hat{H}_1$ and $\hat{H}_2$) was highly significant for all character. It were highly significant for days to flowering, days to maturity, plant height, length of main raceme, number of siliquae per plant, oil content, test weight and seed yield per plant. The estimates of $\hat{H}_1$ were higher than that of the estimates of $\hat{H}_2$ for all characters. It indicates unequal distribution of positive and negative alleles. The dominant components exhibited the prevalence of non-additive gene action for controlling these attributes. All the estimates of $\hat{F}$ (mean of Fr value, where Fr is the proportion of negatives effects of Genes in rth parents) was positive and significant number of siliquae per plant, days to flowering, days to maturity, plant height and except for which is highly significant whereas days to maturity was negative and significant. Indicating the excess of dominant, positive Genes for controlling the characters. The estimates of $\hat{h}^2$ were positive and highly significant for days to flowering, days to maturity, plant height, length of main raceme, oil content, test weight, seed yield per plant. Exhibiting that mean direction of dominance was positive. The values of $\hat{E}$ Component were highly significant for days to maturity. The $\hat{E}$ Values of other traits did not show significance, indicating that these characters were less stable than other characters having environmental inferences and vice-versa. The estimates of mean degree of dominance $(\hat{H}_1/\hat{D})^{0.5}$ were more than unity for length of main raceme, number of secondary branches per plant oil content, test weight and seed yield per plant indicating over dominance in these traits. The proportion of genes with positive and negative effects $(\hat{H}_2/4\hat{H}_1)$ were near or equal to theoretical value (0.25) for all the nine characters indicating that positive and negative genes were symmetrically distributed among the parents for these attributes. The ratio of dominant and recessive alleles, i.e., $(4\hat{D}\hat{H}_1)^{0.5}+\hat{F}/(4\hat{D}\hat{H}_1)^{0.5}$ –F or KD/KR were more than one for days to flowering, days to maturity, plant height, length of main raceme, number of siliquae per plant, number of secondary branches per plant, oil content, test weight and seed yield per plant. While rest of the traits had values less than one which revealed that dominant genes were more frequent than recessive genes in the above eight characters. The ratio $\hat{h}^2/\hat{H}_2$ which measures the group of genes showing dominance was less than unity for all the characters except days to maturity, plant height, oil content, test weight, seed yield per plant. In which more than one gene groups were responsible for the expression of these traits. The coefficient of correlation (r) between parental order of dominance and parental measurements were found negative for length of main raceme, number of siliquae per plant and number of secondary branches per plant, oil content, test weight, seed yield per plant, while it was positive for all other traits. These findings were also similar to Chauhan *et al*. (2008) [14], Upadhyay *et al*. (2009) [18], Sohan Ram and Nutan Verma (2010) [16], Lal *et al*. (2011), Yadav *et al*. (2012) [13], Singh *et al*. (2013) and Shekhawat *et al*. (2014) [12].

Table-1: ANOVA of parents, F_1's and Parent's vs F_1s for 9 characters in a 7 x 7 parental diallel cross of Indian mustard: mean sum of squares.

Source of variation	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Length of main raceme (cm)	No. of Siliquae/ plant
Replications	02	04.08	06.25	10.36	0.01	06.58
Treatments	27	49.93**	78.01**	167.16**	106.92**	1169.86**
Parents	06	102.98**	112.15**	340.76**	175.53**	2280.65**
F_1's	20	33.56**	68.66**	105.71**	70.46**	894.90**
Parents Vs. F_1s	01	59.06**	60.04**	354.75**	424.32**	04.34
Error	54	2.03	2.02	05.13	3.56	16.44

Table 1: Continue…….

Source of variation	d. f.	No. of secondary branches / plant	Oil content (%)	Test weight (g)	Seed yield /plant (g)
Replications	02	3.32	0.17	0.09	4.00
Treatments	27	09.81**	5.57**	0.85**	42.57**
Parents	06	22.52**	3.40**	1.09**	60.09**
F_1's	20	06.16	3.97**	0.07*	33.09**
Parents Vs. F_1s	01	06.67	50.97**	2.10**	127.14**
Error	54	3.51	0.13	0.03	05.71

*Significant at P = 0.05; **Significant at P = 0.01

Table 2: Estimates of bi, SE $_{bi}$ (b-0)/SE $_{bi}$, and t^2 for 9 characters in a 7 x 7 parental diallel cross of Indian mustard.

.	bi	SE $_{bi}$	(b-0)/ SE $_{bi}$	(1-b) / SE $_{bi}$	t^2
Days to flowering	1.0276	0.1221	8.42**	0.23	0.2856
Days to maturity	1.0188	0.0333	30.61**	0.56	0.4264
Plant height (cm)	1.1076	0.1016	10.90**	1.06	1.8760
Length of main raceme (cm)	0.2775	0.2775	1.09	2.51*	0.8885
No. siliquae/ plant	0.6882	0.3044	2.26	1.02	0.0108
No. of secondary branches/plant	0.3236	0.3249	1.00	2.08	0.3198
Oil content (%)	0.4035	0.2401	1.68	2.48	1.3077
Test weight (g)	0.3246	0.1170	2.77*	5.77**	12.4544**
Seed yield / plant (g)	0.8510	0.2264	3.76*	0.66	0.0019

*Significant at p = 0.05, **Significant at p = 0.01

Table 3: Estimates of variance components and related parameters for 9 characters in a 7 x 7 parental diallel crosses in Indian mustard.

Characters	$\hat{D}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{F}$	$\hat{h}^2$	$\hat{E}$	$(\hat{H}_1/\hat{D})^{0.5}$	$\hat{H}_2/4\hat{H}_1$	KD/KR	$\hat{h}^2/\hat{H}_2$	r
Days to flowering	33.65**	16.21**	10.87**	13.11**	10.69**	0.68	0.69	0.17	1.78	0.98	0.78
SE	± 0.76	± 1.83	± 1.61	± 1.82	± 1.08	± 0.27					
Days to maturity	36.71**	6.10**	4.97**	-14.17**	10.87**	0.68**	0.41	0.20	0.36	2.19	0.96
SE	±0.33	± 0.79	± 0.70	± 0.79	±0.47	± 0.12					
Plant height	111.88**	54.45**	48.77**	38.14**	65.36**	1.71	0.70	0.22	1.65	1.34	0.00
SE	±2.58	± 6.22	± 5.48	± 6.19	± 3.68	± 0.91					
Length of main raceme	57.32**	107.80**	80.44**	57.28	78.59**	1.19	1.37	0.19	2.15	0.98	-0.47
SE	±11.01	± 26.50	± 23.35	± 26.41	±15.18	± 3.89					
No. of siliquae/ plant	754.75**	668.51**	435.30*	427.16**	-1.87	5.47	0.94	0.16	1.86	0.00	-0.12
SE	±76.74	± 184.50	± 162.57	±183.85	109.19	± 27.10					
No. of Secondary branches/plant	6.33**	6.81	4.72	6.12	± 0.67	1.17	1.04	0.17	2.74	0.14	-0.66
SE	±01.37	± 3.30	± 2.91	± 3.29	1.95	± 0.48					
Oil content	1.09*	4.72**	3.69*	0.26	9.41**	0.05	2.08	0.20	1.12	2.55	-0.78
SE	±0.41	± 0.99	± 0.87	± 0.99	± 0.69	± 0.15					
Test weight	0.35**	0.43*	0.33*	0.03	0.39**	0.01	1.10	0.19	1.09	1.17	-0.27
SE	±0.04	± 0.11	± 0.09	± 0.11	± 0.06	± 0.02					
Seed yield/plant	18.13**	19.67*	18.36*	2.02	22.79**	1.91	1.04	0.23	1.11	1.24	-0.76
SE	±2.62	± 6.30	± 5.55	± 6.28	± 3.73	± 0.93					

*Significant at P = 0.05; **Significant at P = 0.01

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